-172	10 30 50 GCAGCGGCACGGCAGCAGCGGCAACAAGTGCCGGACTAGCAGAGCCAAGCCGGAGCAGTC	-231
-112	70 90 110 CCTGCCGCCGACACCGCCGGGCCGCCGCCGCGCGCGCGCG	-171
-52	130 150 170 GCGGTCGCCGGGGCCGCGCGCGCGCGCGCGCGCGATCTCCCG	-111
8	190 210 230 CCCTTGCCCCCGCCCGCCGAGCTGGAGCTGCTCCCGGACAAGATATGAGAAATGAGTGT M_S_V	-51 -16
68 23	250 270 290 TGGACGTCGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTATTT	9 4
128 43	310 330 350 TATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGGGAAGTAATAAT <u>I M E V S K S S Q</u> E K N G K G E V I I	69 24
188 63	370 390 410 ACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGGAACCGAGAGCA PKEKFWKISTPPEAYWNREQ	129 44
248 83	430 450 470 AGAGAAGCTGAACCGGCAGTACAACCCCATCCTGAGCATGCTGACCAACCA	189 64
308 103	490 . 510 530 GGCGGCAGCTCTCCAATATAAGCCATCTGAACTACTGCGAACCTGACCTGAGGGTCAC A G R L S N I S H L N Y C E P D L R V T	249 84
368 123	550 570 590 GTCGGTGGTTACGGGTTTTAACAACTTGCCGGACAGATTTAAAGACTTTCTGCTGTATTT S V V T G F N N L P D R F K D F L L Y L	309 104
428 143	610 630 650 GAGATGCCGCAATTATTCACTGCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTT R C R N Y S L L I D Q P D K C A K K P F	369 124
488 163	670 690 710 CTTGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAAGCAA	429 144
548 183	730 750 770 ATCCTGGGGCCAAGAAAGCAACGCAGGAACCAAACGGTGGTGCGAGTCTTCCTGCTGGG SWGQESNAGNQTVVRVFLLG	489 164
608 203	790 810 830 CCAGACACCCCAGAGGACAACCACCCCGACCTTTCAGATATGCTGAAATTTGAGAGTGA Q T P P E D N H P D L S D M L K F E S E	549 184

FIG.1A

	211	
609 204	850 870 890 GAAGCACCAAGACATTCTTATGTGGAACTACAGAGACACTTTCTTCAACTTGTCTCTGAA K H Q D I L M W N Y R D T F F N L S L K	668 223
669 224	910 930 950 GGAAGTGCTGTTTCTCAGGTGGGTAAGTACTTCCTGCCCAGACACTGAGTTTGTTT	728 243
729 244	970 990 1010 GGGCGATGACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATC G D D D V F V N T H H I L N Y L N S L S	788 263
789 264	1030 1050 1070 CAAGACCAAAGCCAAAGATCTCTTCATAGGTGATGTGAT	848 283
849 284	1090 1110 1130 GGATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTCTACCCACCC	908 303
909 304	1150 1170 1190 TGCAGGGGAGGGGGTTCCTCTACTCCGGCCACCTGGCCCTGAGGCTGTACCATATCAC A G G G F L Y S G H L A L R L Y H I T	968 323
969 324	1210 1230 1250 TGACCAGGTCCATCTCTACCCCATTGATGACGTTTATACTGGAATGTGCCTTCAGAAACT DQVHLYPIDDVYTGMCLQKL	1028 343
1029 344	1270 1290 1310 CGGCCTCGTTCCAGAGAAACACAAAGGCTTCAGGACATTTGATATCGAGGAGAAAAACAA G L V P E K H K G F R T F D I E E K N K	1088 363
1089 364	1330 1350 1370 AAATAACATCTGCTCCTATGTAGATCTGATGTTAGTACATAGTAGAAAACCTCAAGAGAT N N I C S Y V D L M L V H S R K P Q E M	1148 383
1149 384	1390 1410 1430 GATTGATATTTGGTCTCAGTTGCAGAGTGCTCATTTAAAATGCTAAAATAGATACAAACT I D I W S Q L Q S A H L K C *	1208 397
1209	1450 1470 1490 CAATTTTGCATAGAAAGGTGTATTTTGAATAGTTCCCATGTTGTGTTCTCACATTAGAGT	1268
1269	1510 1530 1550 AATTTCTATATTAAACCATGAAAATTGCCTTTATGAGTGATACCCATTTGAGGGCCTCTA	1328
1329	1570 1590 1610 AACCCTTCAATTTGGTACTCACGTGAAGAGGGAAAGCGGAAGATGGTAATTTTTTTT	1388
1389	1630 1650 1670 GGATGATATGGCAGGATGATTGGTTCTGATCTTACCGGCTAGTGGTCATTTTTAAAAAAAC	1448
1449	1690 1710 1730 TTGTACCCTCTTATCTGAAATCCTGTTTCTGGAATTTGGCCATTTTAAGTGATTTTGTTT	1508

FIG.1B

1509	1750 1770 1790 GCCCTCTTCTATAATATTCCTACTTCCCATAATAATGACTGATTTATTT	1568
1569	1810 1830 1850 ATTTATAAACCTATTGGCTACAAAGACTTTGTTAAACATTATCCAGTGGTTTTCGTGAAA	1628
1629	1870 1890 1910 TGGAATTATGTTTATTTTATGGGATTTGGGTAAATTTTAAATTGTCTAGAAAACTGAAA	1688
1689	1930 1950 1970 TTTCAGTTGTCAGTTGTGGAATTCAGTTTTTCAATTGTGGAAATTTCCTGCCACCCCAAC	1748
1749	1990 2010 2030 AGTATTTTGTGTGTTAATTAATTTTGCAAAATGAGAATCATGGTGTGACACTCATCTAA	1808
1809	2050 2070 2090 TTTATCTTGTTGATGTTATGGTCATAATAAGGAGAAAGAGGGTTTAATTTTTCTTGTA	1868
1869	2110 2130 2150 TTTGGTTTCCTGGTGGTATCATAGTGTAATTTTAGTATTTGAAAATCAGTGTGATTCCTT	1928
1929	2170 2190 2210 AATGGCCAACTGAAGATTGAATTGCCGCTAACAACCATATCGTGTTAGTGAATTTTCAAT	1988
1989	2230 2250 2270 ATGGACCAGGAAGGCATATGTATTTTGAACTTGAGTGAAAAGGTTGAAGTTACAGACTTT	2048
2049	2290 2310 2330 TGCATAGATGGTTTGTCAATTTAAAATTCCAGAATTTATTATTGCCATATTTTCACATGC	2108
2109	2350 2370 2390 TGCTTATACAAGATTATTATTGAGTAGTAACTGTTCCCTGTCTATGTAGAAGTGCCTGTG	2168
2169	2410 2430 2450 TTTTTATTTATTGTTCCAGATCAAAGACCAAAACATTTTCTTAAATATCTCTTATGTAAT	2228
2229	2470 2490 2510 ATTTTATTTGTATACAGTGTTGTTGATGAAATATTTAACTAGAGCATGATATTTTAAATG	2288
2289	2530 2550 2570 TTAAGGTGTAACATATGTTAAATAAAACTGTTATTTTTGAATTTTAAAATTTGTTTTTTG	2348
2349	2590 2610 2630 GGGGTATGAACTACTAGAGTTTAAAATTCTGCCAAACTATTACTTATATGTACTATTGTG	2408
2409	2650 2670 2690 TAACATACTTTCTTGAAATATTTTTGTTTATAGAATTGAAGGTTCTTATCAGATGGGATA	2468
2469	2710 2730 CTGGGGATTATAAACAATGGAAATAAAGCCACTGTATTTTTAAAA	2513

FIG.1C

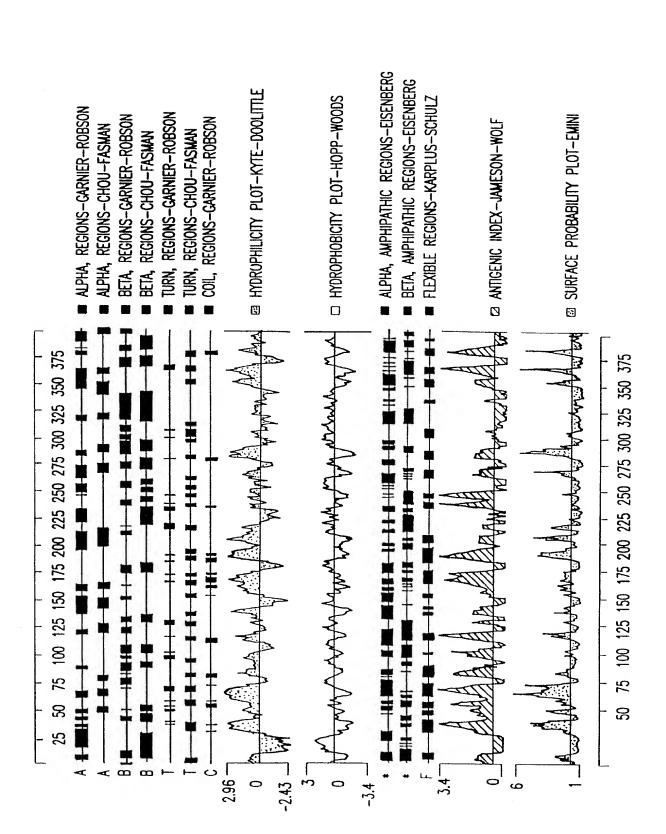
60	NREQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGF	109
2	QSKHRKLLLRCLLVLPLIL.LVDYCGLLTHLHELNF.ERHFHYPLNDDTG	49
110	NNLPDRFKDFLLYLRCRNYSLLIDQPDKCAKKPFLLLAIKSLTPHFAR: : : :	157
50	SGSASSGLDKFAYLRVPSFTAEVPVDQPARLTMLIKSAVGNSRR	93
158	RQAIRESWGQESNAGNQTVVRVFLLGQTPPEDNHPDLSDMLKFESEKHQD	207
94	: . :. :: : : : : . . REAIRRTWGYEGRFSDVHLRRVFLLGTAEDSEKDVAWESREHGD	137
208	ILMWNYRDTFFNLSLKEVLFLRWVSTSCPDTEFVFKGDDDVFVNTHHILN	257
138	ILQADFTDAYFNNTLKTMLGMRWASEQFNRSEFYLFVDDDYYVSAKNVLK	187
258	YLNSLSKTKAKDLFIGDVIHNAGPHRDKKLKYYIPEVVYS.GLYPPYAGG: ::::::::::::::::::::::::::::	306
188	FLGRGRQSHQPELLFAGHVFQTSPLRHKFSKWYVSLEEYPFDRWPPYVTA	237
307	GGFLYSGHLALRLYHITDQVHLYPIDDVYTGMCLQKLGLVPEKHKGFRTF	356
238	GAFILSQKALRQLYAASVHLPLFRFDDVYLGIVALKAGISLQHCDDFRFH	287
357	DIEEKNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHL 395	
288	PDAYKGDDSYSSVIA SHEEGDPEEMTRVWNECRSANY 324	

FIG.2

Dkt. No. 1488.0620002/EKS/GLL; Inventors: SOPPET et al.; Tel: 202/371-2600 Title: Cardiac and Pancreatic Protein and Gene

5/7





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Title: Cardiac and Pancreatic Protein and Gene

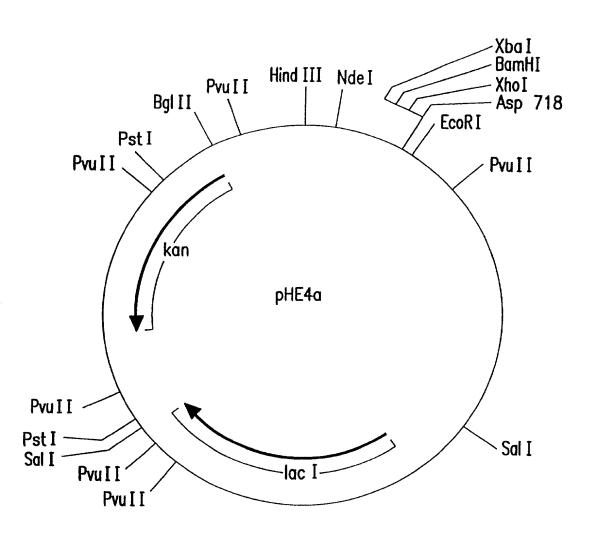


FIG.4

7/7

Operator 1 AAGCTT AAAAACTGCAAAAAATAGTTTGACT -35

Operator 2 50 TAAGATGTACC 10

S/D 94 AGAGGAGAAATTA CATAT F16.5